

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/114,844

OIPE

#10

DATE: 07/21/98
TIME: 14:18:07

INPUT SET: S27566.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Ashkenazi, Avi J.
6 Gurney, Austin
7
8 (ii) TITLE OF INVENTION: RTD Receptor
9
10 (iii) NUMBER OF SEQUENCES: 5
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Genentech, Inc.
14 (B) STREET: 1 DNA Way
15 (C) CITY: South San Francisco
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 94080
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: WinPatin (Genentech)
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:
28 (B) FILING DATE: 14-Jul-1998
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 60/056974
33 (B) FILING DATE: 26-AUG-1997
34
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Marschang, Diane L.
37 (B) REGISTRATION NUMBER: 35,600
38 (C) REFERENCE/DOCKET NUMBER: P1129R1
39
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: 650/225-5416
42 (B) TELEFAX: 650/952-9881
43 (2) INFORMATION FOR SEQ ID NO:1:
44
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 386 amino acids

RAW SEQUENCE LISTING PATENT APPLICATION *US/09/114,844*

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47      (B) TYPE: Amino Acid
48      (D) TOPOLOGY: Linear
49
50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
51
52      Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
53      1          5          10          15
54
55      Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
56      20          25          30
57
58      Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
59      35          40          45
60
61      Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
62      50          55          60
63
64      Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
65      65          70          75
66
67      Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
68      80          85          90
69
70      Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
71      95          100         105
72
73      Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
74      110         115         120
75
76      Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
77      125         130         135
78
79      Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
80      140         145         150
81
82      Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
83      155         160         165
84
85      Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
86      170         175         180
87
88      Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
89      185         190         195
90
91      Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
92      200         205         210
93
94      His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val
95      215         220         225
96
97      Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
98      230         235         240
99

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100  Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His
101              245              250              255
102
103  Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
104              260              265              270
105
106  Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
107              275              280              285
108
109  Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
110              290              295              300
111
112  Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln
113              305              310              315
114
115  Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
116              320              325              330
117
118  Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
119              335              340              345
120
121  Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
122              350              355              360
123
124  Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
125              365              370              375
126
127  Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
128              380              385 386
129

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

141  CCAACTGCAC CTCGGTTCTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG 50
142
143  ATCCCTCGAC CTCGACCCAC GCGTCCGGAA CCTTTGCACG CGCACAAACT 100
144
145  ACGGGGACGA TTTCTGATTG ATTTTGGCG CTTTCGATCC ACCCTCCTCC 150
146
147  CTTCTC  ATG GGA CTT TGG GGA CAA AGC GTC CCG ACC GCC 189
148          Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
149          1          5          10
150
151  TCG AGC GCT CGA GCA GGG CGC TAT CCA GGA GCC AGG ACA 228
152  Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr

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153		15		20	
154					
155	GCG TCG GGA ACC AGA CCA TGG CTC CTG GAC CCC AAG ATC	267			
156	Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile				
157	25 30 35				
158					
159	CTT AAG TTC GTC GTC TTC ATC GTC GCG GTT CTG CTG CCG	306			
160	Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro				
161	40 45 50				
162					
163	GTC CGG GTT GAC TCT GCC ACC ATC CCC CGG CAG GAC GAA	345			
164	Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu				
165	55 60				
166					
167	GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG AGG CGC	384			
168	Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg				
169	65 70 75				
170					
171	AGC CTC AAG GAG GAG GAG TGT CCA GCA GGA TCT CAT AGA	423			
172	Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg				
173	80 85				
174					
175	TCA GAA TAT ACT GGA GCC TGT AAC CCG TGC ACA GAG GGT	462			
176	Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly				
177	90 95 100				
178					
179	GTG GAT TAC ACC ATT GCT TCC AAC AAT TTG CCT TCT TGC	501			
180	Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys				
181	105 110 115				
182					
183	CTG CTA TGT ACA GTT TGT AAA TCA GGT CAA ACA AAT AAA	540			
184	Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys				
185	120 125				
186					
187	AGT TCC TGT ACC ACG ACC AGA GAC ACC GTG TGT CAG TGT	579			
188	Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys				
189	130 135 140				
190					
191	GAA AAA GGA AGC TTC CAG GAT AAA AAC TCC CCT GAG ATG	618			
192	Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met				
193	145 150				
194					
195	TGC CGG ACG TGT AGA ACA GGG TGT CCC AGA GGG ATG GTC	657			
196	Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val				
197	155 160 165				
198					
199	AAG GTC AGT AAT TGT ACG CCC CGG AGT GAC ATC AAG TGC	696			
200	Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys				
201	170 175 180				
202					
203	AAA AAT GAA TCA GCT GCC AGT TCC ACT GGG AAA ACC CCA	735			
204	Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro				
205	185 190				

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206															
207	GCA	GCG	GAG	GAG	ACA	GTG	ACC	ACC	ATC	CTG	GGG	ATG	CTT	774	
208	Ala	Ala	Glu	Glu	Thr	Val	Thr	Thr	Ile	Leu	Gly	Met	Leu		
209		195					200					205			
210															
211	GCC	TCT	CCC	TAT	CAC	TAC	CTT	ATC	ATC	ATA	GTG	GTT	TTA	813	
212	Ala	Ser	Pro	Tyr	His	Tyr	Leu	Ile	Ile	Ile	Val	Val	Leu		
213				210						215					
214															
215	GTC	ATC	ATT	TTA	GCT	GTG	GTT	GTG	GTT	GGC	TTT	TCA	TGT	852	
216	Val	Ile	Ile	Leu	Ala	Val	Val	Val	Val	Gly	Phe	Ser	Cys		
217	220					225					230				
218															
219	CGG	AAG	AAA	TTC	ATT	TCT	TAC	CTC	AAA	GGC	ATC	TGC	TCA	891	
220	Arg	Lys	Lys	Phe	Ile	Ser	Tyr	Leu	Lys	Gly	Ile	Cys	Ser		
221			235					240					245		
222															
223	GGT	GGT	GGA	GGA	GGT	CCC	GAA	CGT	GTG	CAC	AGA	GTC	CTT	930	
224	Gly	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Val	His	Arg	Val	Leu		
225					250					255					
226															
227	TTC	CGG	CGG	CGT	TCA	TGT	CCT	TCA	CGA	GTT	CCT	GGG	GCG	969	
228	Phe	Arg	Arg	Arg	Ser	Cys	Pro	Ser	Arg	Val	Pro	Gly	Ala		
229		260					265					270			
230															
231	GAG	GAC	AAT	GCC	CGC	AAC	GAG	ACC	CTG	AGT	AAC	AGA	TAC	1008	
232	Glu	Asp	Asn	Ala	Arg	Asn	Glu	Thr	Leu	Ser	Asn	Arg	Tyr		
233				275					280						
234															
235	TTG	CAG	CCC	ACC	CAG	GTC	TCT	GAG	CAG	GAA	ATC	CAA	GGT	1047	
236	Leu	Gln	Pro	Thr	Gln	Val	Ser	Glu	Gln	Glu	Ile	Gln	Gly		
237	285					290					295				
238															
239	CAG	GAG	CTG	GCA	GAG	CTA	ACA	GGT	GTG	ACT	GTA	GAG	TYG	1086	
240	Gln	Glu	Leu	Ala	Glu	Leu	Thr	Gly	Val	Thr	Val	Glu	Xaa		
241			300					305					310		
242															
243	CCA	GAG	GAG	CCA	CAG	CGT	CTG	CTG	GAA	CAG	GCA	GAA	GCT	1125	
244	Pro	Glu	Glu	Pro	Gln	Arg	Leu	Leu	Glu	Gln	Ala	Glu	Ala		
245					315					320					
246															
247	GAA	GGG	TGT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GTG	AAT	1164	
248	Glu	Gly	Cys	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Val	Asn		
249		325					330					335			
250															
251	GAC	GCT	GAC	TCC	GCT	GAC	ATC	AGC	ACC	TTG	CTG	GAT	GCC	1203	
252	Asp	Ala	Asp	Ser	Ala	Asp	Ile	Ser	Thr	Leu	Leu	Asp	Ala		
2															

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/114,844

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Original Text